

**IN THE CLAIMS:**

Please amend claims 5-6, 8, 12 and 14-15 as follows:

1. (Previously Presented) A method for displaying a dendrogram comprising the steps of:
  - clustering a plurality of biopolymers with a first clustering method which is based on a set of gene expression data obtained by experiments on the plurality of biopolymers, and displaying clustering results thereof in a form of a dendrogram in a display window;
  - selecting a subtree in the dendrogram in the display window;
  - displaying the selected subtree in a separate display window;
  - grouping biopolymers in the selected subtree in the separate display window into at least one function group sharing one of functional characteristics consisting of enzymatic, metabolic, transporting, and cell cycle functions; and
  - displaying said function group of biopolymers in the separate display window.
2. (Previously Presented) A method for displaying a dendrogram according to claim 1, further comprising a step of:
  - designating a second clustering method, which is different from the first clustering method, for further clustering the biopolymers in the selected subtree in the separate display window.
3. (Previously Presented) A method for displaying a dendrogram comprising the steps of:
  - clustering a plurality of biopolymers based on a set of gene expression data obtained by experiments on the plurality of biopolymers, and displaying clustering results thereof in a form of a dendrogram in a display window;
  - selecting a subtree in the dendrogram in the display window;
  - replacing the selected subtree with an icon in the dendrogram thereby displaying the dendrogram with the icon rather than with the selected subtree;
  - grouping biopolymers in the simplified presentation in the display window into at least one function group sharing one of functional characteristics consisting of

enzymatic, metabolic, transporting, and cell cycle functions; and

displaying said function group of biopolymers in the simplified presentation in the display window.

4. (Previously Presented) A method for displaying a dendrogram according to claim 3, further comprising a step of restoring the selected subtree back from the replacing icon in the dendrogram in the display window.
5. (Currently Amended) A method for displaying a dendrogram comprising the steps of:
  - clustering a plurality of biopolymers based on a set of gene expression data obtained by experiments on the plurality of biopolymers, and displaying clustering results thereof in a form of a dendrogram in a display window;
  - selecting a subtree in the dendrogram in the display window;
  - searching within ~~biopolymer~~ attribute information of biopolymers contained in the selected subtree for keywords available in a keyword dictionary file; and
  - counting biopolymers in the selected subtree whose ~~biopolymer~~ attribute information contains at least one of the searched keywords and displaying each of the searched keywords with a corresponding count of the biopolymers whose ~~biopolymer~~ attribute information contains at least one of the searched keywords;
  - grouping biopolymers in the selected subtree into at least one function group sharing one of functional characteristics consisting of enzymatic, metabolic, transporting, and cell cycle functions;
  - displaying said function group of biopolymers in the display window; and
  - displaying the searched keywords available in the selected subtree and said count in a separated display window on top of the display window displaying said function group of biopolymers therein;
  - highlighting in the display window a location of each of the biopolymers in the selected subtree whose ~~biopolymer~~ attribute information contains the searched keywords;
  - displaying the highlighted keywords together with said function group of biopolymers thereby confirming biopolymers sharing said one of said functional characteristics are grouped in the selected subtree,
  - wherein said ~~biopolymer~~ attribute information includes a unique nucleotide

sequence identifier and a description of a corresponding nucleotide sequence, said description includes a source organism, a gene name/protein name, or a function.

6. (Currently Amended) A method for displaying a dendrogram comprising the steps of:
  - clustering a plurality of biopolymers based on a set of gene expression data obtained by experiments on the plurality of biopolymers, and displaying clustering results thereof in a form of a dendrogram in a display window;
  - selecting a subtree in the dendrogram in the display window;
  - designating at least one keyword from a keyword dictionary file;
  - searching within ~~biopolymer~~ attribute information of biopolymers contained in the selected subtree for biopolymers whose ~~biopolymer~~ attribute information contains the designated keyword; and
  - highlighting in the display window a location of each of the biopolymers in the selected subtree whose ~~biopolymer~~ attribute information contains the designated keyword;
  - grouping biopolymers in the selected subtree into at least one function group sharing one of functional characteristics consisting of enzymatic, metabolic, transporting, and cell cycle functions;
  - displaying the highlighted keywords together with said function group of biopolymers in the display window thereby confirming biopolymers sharing said one of said functional characteristics are grouped in the selected subtree,
  - wherein said ~~biopolymer~~ attribute information includes a unique nucleotide sequence identifier and a description of a corresponding nucleotide sequence, said description includes a source organism, a gene name/protein name, or a function.
7. (Original) A method for displaying a dendrogram according to any one of claims 1 to 6, wherein the biopolymers are cDNAs, RNAs, DNA fragments or genes.
8. (Currently Amended) A system for displaying a dendrogram comprising:
  - a clustering processor for clustering a plurality of biopolymers based on a set of gene expression data obtained by experiments on the plurality of biopolymers, and analyzing and displaying clustering results thereof in a form of a dendrogram in a display window;

a display system for displaying the dendrogram, for displaying on a separate window a subtree selected by a user in the display window thereby grouping biopolymers in the selected subtree in the separate display window into at least one function group sharing one of functional characteristics consisting of enzymatic, metabolic, transporting, and cell cycle functions, and for displaying said function group of biopolymers in the separate display window; and

a keyword dictionary file for storing keywords of ~~biopolymer~~ attribute information associated with each of the plurality of biopolymers, said ~~biopolymer~~ attribute information including a unique nucleotide sequence identifier and a description of a corresponding nucleotide sequence, said description includes a source organism, a gene name/protein name, or a function.

9. (Previously Presented) A system for displaying a dendrogram according to claim 8, further comprising input means for selecting the subtree by the user.
10. (Previously Presented) A system for displaying a dendrogram according to claim 8, further comprising means for designating a different clustering method for said grouping biopolymers in the selected subtree displayed on the separate window to secondarily cluster biopolymers included in the subtree, wherein the display system displays secondarily clustered biopolymers in the selected subtree in a form of a dendrogram.
11. (Previously Presented) A system for displaying a dendrogram according to any one of claims 8 to 10, further comprising means for replacing the selected subtree with an icon, and means for restoring the selected subtree back from the replacing icon in the dendrogram in the display window.
12. (Currently Amended) A system for displaying a dendrogram according to any one of claims 8 to 10, further comprising means for designating keywords from the keyword dictionary file, means for searching within ~~biopolymer~~ attribute information of biopolymers contained in the selected subtree for biopolymers whose ~~biopolymer~~ attribute information contains at least one of the designated keywords, means for counting biopolymers in the subtree whose ~~biopolymer~~ attribute information contains

at least one of the designated keywords, wherein the display system displays each of the designated keywords with a corresponding count of the biopolymers whose ~~biopolymer~~ attribute information contains at least one of the designated keywords, and highlights a location of each of the biopolymers in the selected subtree whose ~~biopolymer~~ attribute information contains at least one of the designated keywords.

13. (Previously Presented) A system for displaying a dendrogram according to any one of claims 8 to 10, wherein the biopolymers are cDNAs, RNAs, DNA fragments or genes.
14. (Currently Amended) A method for displaying a dendrogram according to claim 5, wherein the counting step involves counting biopolymers in the selected subtree whose ~~biopolymer~~ attribute information contains synonyms of said one of the selected keywords.
15. (Currently Amended) A system for displaying a dendrogram according to claim 12, wherein the means for counting counts biopolymers in the selected subtree whose ~~biopolymer~~ attribute information contains synonyms of each of the designated keywords.